

Book reviews

Quantum Evolution: The New Science of Life. Johnjoe McFadden. HarperCollins, London. 2000. Pp. 338. Price £16.99, hardback. ISBN 0 00 255948 X.

Quantum Evolution: The New Science of Life simply does not work. The author has a central idea regarding how Darwinian natural selection may be complemented by another evolutionary force, which he refers to as quantum evolution. However, this idea is hidden in the shortest chapter, near the end of the book, after more than 200 pages of wide-ranging material covering a miscellany of rather tenuously linked subjects — biospheric extremes, reproduction, the origin of life, muscle action, enzyme action and quantum mechanics. This results in the reader becoming progressively frustrated as the book does not get to the point and when one eventually gets there one is in no mood to take on board speculative and badly explained new mechanisms, which is how I viewed the core ideas when I finally reached them.

So, what is McFadden's 'Quantum Evolution', which he describes in his sub-title as 'The New Science of Life'? Firstly, it bears no relation to G. G. Simpson's 'quantum evolution' that we are all familiar with — indeed, and bizarrely, McFadden seems entirely unaware of this standard usage of his key term. There are no references to Simpson's work anywhere in the book. Instead, McFadden's 'quantum evolution' emerges as an application of quantum mechanics to mechanisms of mutation and it becomes, among other things, a proposed way in which the controversial 'adaptive mutations' described in *E. coli* by Cairns *et al.* (1988) might come about. As I have never believed that environmental conditions systematically cause mutations that are adaptive in those conditions, I was not particularly interested in a possible mechanism for the production of such mutations. Perhaps other readers with different preconceptions may take a more positive view.

Regrettably, the recurrent errors throughout the book lead to the feeling of not being in a safe pair of hands. Some of these are trivial, yet add to the general sense of insecurity — for example, a tendency to get names wrong. So, for example, Margulis becomes Margolis, Eldredge becomes Eldridge and Galilei becomes Galiliei. More importantly, there are other parts of the book that are just plain wrong. For example, McFadden says (p. 133) that the second law of thermodynamics 'states that everything in the universe is accompanied by an increase in entropy'. Even the author himself realises that this is not so, because he states on the following page that the second law 'does not forbid processes that decrease entropy', so the first statement represents careless writing rather than misconception. The lesser of two evils, to be sure, but disconcerting nonetheless.

As will be clear by now, I did not like the central idea or the book as a whole. However, I was left asking myself whether I

might have been prepared to consider the central idea more sympathetically if McFadden had written a much shorter book with quantum evolution up front and with greater attention to detail. I suspect the answer is no.

References

CAIRNS, J., OVERBAUGH, J. AND MILLER, S. 1988. The origin of mutants. *Nature*, **335**, 142–145.

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The Human Inheritance: Genes, Language, and Evolution. Bryan Sykes (ed.). Oxford University Press, Oxford. 1999. Pp. 195. Price £19.99, hardback. ISBN 0 19 850274 5.

During the spring of 1997, Wolfson College, Oxford, held a series of eight lectures on human origins, evolution and diversity, which are now published in this compact book. Bryan Sykes, the organiser of these lectures, did not set out with the intention of publishing them but I am glad that he changed his mind. The contributors, Colin Renfrew, Chris Stringer, Don Ringe, Gabriel Dover, Bryan Sykes, Svante Pääbo, Ryk Ward and Walter Bodmer have produced a set of exciting and thought-provoking essays. Although I was already familiar with some of the more genetic material it was the essays, which included linguistics, palaeontology and human migrations — topics that I rarely have the time to read about in any depth — that really grabbed my attention. Also, it is always interesting to find that other disciplines are driven with the same types of strong disagreements and controversies about approaches, methods and, even, the data that afflict one's own field.

Whilst it might be invidious to single out individual essays as they are universally excellent, it was those where my knowledge of the field was minimal that gave me the most enjoyment, for example, Svante Pääbo's 'warts and all' description of the problems and frustrations of working on ancient DNA. If I was not aware before I read these essays that there is probably a limit to how far origins of languages can be traced because of the way languages are transmitted and evolve, I certainly am now. Similarly, despite the considerable hype around studies of ancient DNA in the press and media, Pääbo's statement that '...there probably is a time barrier, which I would put between 100,000 and 1,000,000 years, that we will not be able to break with ancient DNA' was refreshingly frank.

This is a thoroughly enjoyable book — I must have read it, in its entirety, at least three times. It makes excellent bedtime and travel reading. All I can really do is recommend it most highly — read and enjoy.

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DNA Profiling and DNA Fingerprinting. Jörg T. Epplen and Thomas Lubjuhn (eds). Birkhäuser Verlag, Basel. 1999. Pp. 252. Price SFr. 128 (DM 148), spiral-bound paperback. ISBN 3 7643 6018 6.

Two key advances have underlain the recent revolution in molecular biology that have impacted on diverse disciplines such as forensics, veterinary medicine, disease detection and monitoring, genetic mapping, population genetics and molecular ecology. Firstly, the discovery of hypervariable DNA sequences, and secondly, the advent of the Polymerase Chain Reaction (PCR), which when combined can provide an informative and typically robust approach to characterize genomes by developing a DNA fragment band (allele) pattern. This multi-authored text by Epplen and Lubjuhn, published within the Birkhäuser Verlag series, *Methods and Tools in Biosciences and Medicine*, focuses on the diverse applications of probe and PCR-based genetic fingerprinting which encompass studies on prokaryotes, plants and animals.

The book covers sufficient diversity and applications to be at home in almost any molecular-based laboratory. It is essentially a hands-on practical guide with a focus on methodology and statistical aspects of several divergent technologies, including multilocus fingerprinting, oligonucleotide fingerprinting, microsatellite analysis, amplified fragment length polymorphisms (AFLP), and two-dimensional fingerprinting. Each chapter is organised in a user-friendly format with a brief introduction, a compilation of clear, point-by-point protocols, and a consideration of pertinent applications to illustrate respective pros and cons, concluding with a variously developed section on trouble-shooting.

In an age of ever-expanding technologies and the associated remorseless proliferation of practical manuals what is distinctive about this volume? Firstly, it is unusual in its diversity of applications, both in terms of taxonomic coverage as well as the range of questions tackled. In the 15 chapters presented there are, for example, valuable considerations of the specific genomic characteristics of plants and prokaryotes, and how these influence the choice of fingerprinting procedure and statistical analysis of data. It covers the use of genetic fingerprinting in behavioural ecology, with particular reference to birds and insects, veterinary medicine, multifactorial disease detection in humans using single nucleotide polymorphisms, and the value of employing DNA profiling of human Y chromosomes. Secondly, although there is the usual extent of author-based variation in style the approach adopted is question-led. Thus, not only does it emphasise that no single

marker system is appropriate for all questions but usefully provides advice on how to maximise the genetic signal relative to background noise in relation to the scale of enquiry. The most appropriate approaches for tackling questions of parentage, relatedness, clonal, population and species-level problems are considered although the depth of coverage varies significantly between chapters. For example, the relative value of multilocus vs. single locus approaches for estimating genetic relatedness is well covered among chapters, although the problem of how to deal with between-gel comparisons in the former is given scant attention. Thirdly, there is a refreshing and useful emphasis on statistical analysis of data with valuable reference to appropriate software and availability from published works and the Internet. Although most chapters make some reference to data analysis there are two chapters which stand out. Schlötterer and Zangerl provide a stimulating account of the use of imperfect microsatellites in population genetic analysis, pointing out their higher information content derived from a typically larger number of discernible alleles, although they caution against the labour-intensive procedures to obtain the data and uncertainties regarding interpretation of results. There is also a useful summary by Melo dos Santos on the population genetic analysis of microsatellite data with a valuable consideration of how alternative mutation models influence the choice of test to adopt and a table summarizing the available software programmes.

For balance, there are some shortcomings. Although the text is likely to be most useful to those who actually work in the laboratory as opposed to those (like myself) who wish they had the time to, the potentially strongest asset of trouble-shooting is only variously developed. For example, the chapters on the use of microsatellite analysis in veterinary medicine and two-dimensional fingerprinting provide useful summary tables of symptom and remedy, whereas in seven out of the 15 chapters the reader is referred either to the literature for further details, or to the body of the respective chapter. Although it is understandably more efficient to discuss various technical difficulties while describing the respective procedures, a summary of the most common methodological problems given at the end of each chapter would have better complemented the practical detail provided. There is also an element of restriction of applicability of some protocols, for example, the description of gene mapping which relies heavily on the use of a specific model of apparatus. Finally, in view of the extensive range of topics covered and the unavoidable novelty of several sections to many readers, an informative abstract at the beginning of each chapter would have been an asset in assigning context and utility.

On balance however, *DNA Profiling and DNA Fingerprinting* does provide a highly useful manual for all those involved practically in genetic fingerprinting, and yet there is sufficient coverage of theory, application and data analysis to render the book of value to those of us who merely write about it.

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